

SEQUENCE LISTING

<110> SMITHKLINE BEECHAM CORPORATION
SMITHKLINE BEECHAM plc

<120> METHODS OF MODULATING FABH ACTIVITY

<130> GM50050

<140> TO BE ASSIGNED

<141> 2000-05-04

<150> US 60/132,714

<151> 1999-05-06

<160> 4

<170> FastSEQ for Windows Version 3.0

<210> 1

<211> 942

<212> DNA

<213> Staphylococcus aureus

<400> 1

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gaaagacatt gggcagatga cgatcaagat acttcagatt tagcatatga agcaagtgtg	180
aaagcaatcg ctgacgctgg tattcagcct gaagatatag atatgataat tgttgccaca	240
gcaactggag atatgccatt tccaactgtc gcaaatatgt tgcaagaacg ttaggggacg	300
ggcaaagttg cctctatgga tcaacttgca gcatgttctg gatttatgta ttcaatgatt	360
acagctaaac aatatgttca atctggagat tadcataata ttttagttgt cgggtgcagat	420
aaattatcta aaataacaga tttaactgac cgttctactg cagttctatt tggagatggt	480
gcaggtgctg ttatcatcgg tgaagtttca gaaggcagag gtattataag ttatgaaatg	540
ggttctgatg gcaactggtg taaacattta tathtagata aagatactgg taaactgaaa	600
atgaatggtc gagaagtatt taaatttgct gttagaatta tgggtgatgc atcaacacgt	660
gtagttgaaa aagcgaattt aacatcagat gatatagatt tatattatcc tcatcaagct	720
aatattagaa ttatggaatc agctagagaa cgcttaggta tttcaaaaga caaatgagt	780
gtttctgtaa ataaatatgg aaatacttca gctgcgtcaa tacctttaag tatcgatcaa	840
gaattaaaaa atggtaaact caaagatgat gatacaattg ttcttgctcg attcgggtggc	900

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942

<210> 2

<211> 313

<212> PRT

<213> Staphylococcus aureus

<400> 2

Met Asn Val Gly Ile Lys Gly Phe Gly Ala Tyr Ala Pro Glu Lys Ile
 1 5 10 15
 Ile Asp Asn Ala Tyr Phe Glu Gln Phe Leu Asp Thr Ser Asp Glu Trp
 20 25 30
 Ile Ser Lys Met Thr Gly Ile Lys Glu Arg His Trp Ala Asp Asp Asp
 35 40 45
 Gln Asp Thr Ser Asp Leu Ala Tyr Glu Ala Ser Val Lys Ala Ile Ala
 50 55 60
 Asp Ala Gly Ile Gln Pro Glu Asp Ile Asp Met Ile Ile Val Ala Thr
 65 70 75 80
 Ala Thr Gly Asp Met Pro Phe Pro Thr Val Ala Asn Met Leu Gln Glu
 85 90 95
 Arg Leu Gly Thr Gly Lys Val Ala Ser Met Asp Gln Leu Ala Ala Cys
 100 105 110
 Ser Gly Phe Met Tyr Ser Met Ile Thr Ala Lys Gln Tyr Val Gln Ser
 115 120 125
 Gly Asp Tyr His Asn Ile Leu Val Val Gly Ala Asp Lys Leu Ser Lys
 130 135 140
 Ile Thr Asp Leu Thr Asp Arg Ser Thr Ala Val Leu Phe Gly Asp Gly
 145 150 155 160
 Ala Gly Ala Val Ile Ile Gly Glu Val Ser Glu Gly Arg Gly Ile Ile
 165 170 175
 Ser Tyr Glu Met Gly Ser Asp Gly Thr Gly Gly Lys His Leu Tyr Leu
 180 185 190
 Asp Lys Asp Thr Gly Lys Leu Lys Met Asn Gly Arg Glu Val Phe Lys
 195 200 205
 Phe Ala Val Arg Ile Met Gly Asp Ala Ser Thr Arg Val Val Glu Lys
 210 215 220
 Ala Asn Leu Thr Ser Asp Asp Ile Asp Leu Phe Ile Pro His Gln Ala
 225 230 235 240
 Asn Ile Arg Ile Met Glu Ser Ala Arg Glu Arg Leu Gly Ile Ser Lys
 245 250 255
 Asp Lys Met Ser Val Ser Val Asn Lys Tyr Gly Asn Thr Ser Ala Ala
 260 265 270

Ser Ile Pro Leu Ser Ile Asp Gln Glu Leu Lys Asn Gly Lys Leu Lys
 275 280 285
 Asp Asp Asp Thr Ile Val Leu Val Gly Phe Gly Gly Gly Leu Thr Trp
 290 295 300
 Gly Ala Met Thr Ile Lys Trp Gly Lys
 305 310

<210> 3
 <211> 975
 <212> DNA
 <213> Streptococcus pneumoniae

<400> 3

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cacgacttggt ctcagattat ggataccaat gatgagtggg tttcaagtcg aacgggaata	120
cgacaaaggc atattttcaag aacagaatct accagtgatt tggctacaga gggttgctaag	180
aaactgatgg caaaagctgg aataacagga aaagaactgg attttatcat cctagctacc	240
attactccag attcgatgat gccctctaca gctgctcgtg ttcaagctaa tattggcgct	300
aataaagcct ttgcttttga cttaaccgag gcttgcaagt gatttgtatt tgctctttca	360
actgctgaaa agtttatcgc ttctgggtcgc tttcaaaaag gcttggtgat tggtagtgaa	420
accctctcta aggcagtcga ttggtcggat cgatcaacag ctgtgttggt tggagatggt	480
gctgggtggtg tcttggttaga agctagcgag caagagcatt tcttagctga gagtcttaac	540
agcgatggaa gtcgcagcga gtgtttaact tatgggcatt caggtttgca ttctccattt	600
tcagatcaag aaagtgcaga ttcgtttttg aagatggatg gacgcacagt ctttgatttt	660
gccattcgag atgtagccaa gtctatcaag cagactattg atgaatctcc tatagagggtg	720
acagacttgg attatctgct acttcatcaa gccaatgacc gtatttttga taagatggct	780
agaaaaattg gtgttgaccg agccaaactt ccagccaata tgatggaata tggcaataacc	840
agtgcagcca gtatcccgat tttactttca gagtgtgtag aacaaggctc catcccttta	900
gatggtagcc agactgttct tctatcaggc ttcggtggag gcttgacctg gggcacgctc	960
attcttacaa ttttag	975

<210> 4
 <211> 324
 <212> PRT
 <213> Streptococcus pneumoniae

<400> 4

Met Ala Phe Ala Lys Ile Ser Gln Val Ala His Tyr Val Pro Glu Gln
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 Val Val Thr Asn His Asp Leu Ala Gln Ile Met Asp Thr Asn Asp Glu
 20 25 30
 Trp Ile Ser Ser Arg Thr Gly Ile Arg Gln Arg His Ile Ser Arg Thr

35	40	45
Glu Ser Thr Ser Asp Leu Ala Thr Glu Val Ala Lys Lys Leu Met Ala		
50	55	60
Lys Ala Gly Ile Thr Gly Lys Glu Leu Asp Phe Ile Ile Leu Ala Thr		
65	70	75
Ile Thr Pro Asp Ser Met Met Pro Ser Thr Ala Ala Arg Val Gln Ala		
85	90	95
Asn Ile Gly Ala Asn Lys Ala Phe Ala Phe Asp Leu Thr Ala Ala Cys		
100	105	110
Ser Gly Phe Val Phe Ala Leu Ser Thr Ala Glu Lys Phe Ile Ala Ser		
115	120	125
Gly Arg Phe Gln Lys Gly Leu Val Ile Gly Ser Glu Thr Leu Ser Lys		
130	135	140
Ala Val Asp Trp Ser Asp Arg Ser Thr Ala Val Leu Phe Gly Asp Gly		
145	150	155
Ala Gly Gly Val Leu Leu Glu Ala Ser Glu Gln Glu His Phe Leu Ala		
165	170	175
Glu Ser Leu Asn Ser Asp Gly Ser Arg Ser Glu Cys Leu Thr Tyr Gly		
180	185	190
His Ser Gly Leu His Ser Pro Phe Ser Asp Gln Glu Ser Ala Asp Ser		
195	200	205
Phe Leu Lys Met Asp Gly Arg Thr Val Phe Asp Phe Ala Ile Arg Asp		
210	215	220
Val Ala Lys Ser Ile Lys Gln Thr Ile Asp Glu Ser Pro Ile Glu Val		
225	230	235
Thr Asp Leu Asp Tyr Leu Leu Leu His Gln Ala Asn Asp Arg Ile Leu		
245	250	255
Asp Lys Met Ala Arg Lys Ile Gly Val Asp Arg Ala Lys Leu Pro Ala		
260	265	270
Asn Met Met Glu Tyr Gly Asn Thr Ser Ala Ala Ser Ile Pro Ile Leu		
275	280	285
Leu Ser Glu Cys Val Glu Gln Gly Leu Ile Pro Leu Asp Gly Ser Gln		
290	295	300
Thr Val Leu Leu Ser Gly Phe Gly Gly Gly Leu Thr Trp Gly Thr Leu		
305	310	315
Ile Leu Thr Ile		320